

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 1999, 01:52:19 : Search time 16.06 Seconds

(without alignments)
1283.756 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 1785

Sequence: 1 MGSASPGLSVSPSHLLP.....GIKKPDISORLYQFVHP1 335

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

1: SP_ARCHES: *
2: SP_BACTERIA: *
3: SP_FUNGI: *
4: SP_HUMAN: *
5: SP_INVERTEBRATE: *
6: SP_MAMMAL: *
7: SP_MHC: *
8: SP_ORGANELLE: *
9: SP_PHAGE: *
10: SP_PLANT: *
11: SP_RODENT: *
12: SP_VIRUS: *
13: SP_VERTEBRATE: *
14: SP_UNCLASSIFIED: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	335	4	095238
2	487.5	27.3	363	5	097145
3	417	23.4	532	5	019695
4	299	16.8	255	4	095175
5	288	16.1	253	11	092286
6	283	15.9	336	6	062804
7	274	15.4	432	13	093425
8	265.5	14.9	435	13	09YH25
9	257	14.4	581	4	015723
10	256.5	14.4	300	11	070273
11	255.5	14.3	440	13	09YH05
12	252.5	14.1	481	5	017057
13	248.5	14.0	385	4	014319
14	249	13.9	348	4	099718
15	245	13.7	663	4	099607
16	245	13.7	663	4	060435
17	245	13.7	426	6	062803
18	242	13.6	521	4	015725
19	242	13.6	655	11	092204
20	241	13.5	533	4	015724
21	239	13.4	471	13	057566
22	238.5	13.4	371	4	P78545
23	235.5	13.2	371	11	035275
24	230.5	12.9	490	13	09YH24
25	229	12.8	494	13	057586
26	225	12.6	390	13	09YH8
27	224	12.5	95	4	095058
28	221	12.4	336	13	09YH5
29	219	12.3	454	4	075849

30	218.5	12.2	441	5	027378	027378 caenorhabd
31	218	12.2	428	4	075606	075606 homo sapien
32	213.5	12.0	477	13	09YH6	09YH6 gallus gall
33	212.5	11.9	477	13	093122	093122 xenopus lae
34	209.5	11.7	236	13	09YH7	09YH7 gallus gall
35	207	11.6	788	5	096416	096416 drosophila
36	203	11.4	538	5	093320	093320 caenorhabd
37	201.5	11.3	559	5	026645	026645 strongyloe
38	197.5	11.1	268	13	091744	091744 xenopus lae
39	191	10.7	196	4	016203	016203 homo sapien
40	185	10.4	254	4	016199	016199 homo sapien
41	184	10.3	377	5	022355	022355 caenorhabd
42	182.5	10.2	340	11	070132	070132 rattus norv
43	179	10.0	238	4	099581	099581 homo sapien
44	176	9.9	208	5	018579	018579 caenorhabd
45	155.5	8.7	256	13	042415	042415 gallus gall

ALIGNMENTS

RESULT 1
ID 095238 PRELIMINARY: PRT: 335 AA.
AC 095238:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ETS TRANSCRIPTION FACTOR PDEF.
GN PDEF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA BOETTGER P., FINGER E., AKBARALI Y., THAKRONGSAK U., DUBE A.,
RA BOLTAX J., BROWN L., KUNSCHE C., LIBERMANN T.A.;
RT "Isolation and characterization of a novel prostate
RT epithelium-specific Ets transcription factor, PDEF".
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF071538; AAC95296.1; -
SQ SEQUENCE 335 AA; 37517 MW; 874A5DE8 CRC32;

Query Match	Best Local Similarity	Score	DB ID	Length
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%;	1785;	DB 4;	335;
1 MGSASPGLSVSPSHLLPDTVSRTGLEKAAAGAVGERDMSPPATPEOGLSAFYL 60	100.0%;	1785;	DB 4;	335;
1 SYFDMLYEDSSMAKAPGASSREPEPEQCPYDSQAPAGSLDLPVGLTLEHSL 120	100.0%;	1785;	DB 4;	335;
61 SYFDMLYEDSSMAKAPGASSREPEPEQCPYDSQAPAGSLDLPVGLTLEHSL 120	100.0%;	1785;	DB 4;	335;
121 OVOSAVVEVLTAKLNTADPMDSVNVOKLLTTHOYRLPVGKAFQELAG 180	100.0%;	1785;	DB 4;	335;
121 OVOSAVVEVLTAKLNTADPMDSVNVOKLLTTHOYRLPVGKAFQELAG 180	100.0%;	1785;	DB 4;	335;
181 KELCMSEDFRSPGLGVDLHAHLDTWKAAMKERTSGAIHYCASTEESDTSEV 240	100.0%;	1785;	DB 4;	335;
181 KELCMSEDFRSPGLGVDLHAHLDTWKAAMKERTSGAIHYCASTEESDTSEV 240	100.0%;	1785;	DB 4;	335;
241 DSSCGQPIHLMOFKELLKPHSYGRIRLWLNKKGIFKIEDSAOVARLNGIRKRRPAM 300	100.0%;	1785;	DB 4;	335;
241 DSSCGQPIHLMOFKELLKPHSYGRIRLWLNKKGIFKIEDSAOVARLNGIRKRRPAM 300	100.0%;	1785;	DB 4;	335;
301 NYDKLSRSIRIOTYKKGITRKPDISORLYQFVHP1 335	100.0%;	1785;	DB 4;	335;
301 NYDKLSRSIRIOTYKKGITRKPDISORLYQFVHP1 335	100.0%;	1785;	DB 4;	335;

RA BOFFIELD J., BURTON J., CONNELL M., COPEST T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., ELLIOT L.,
 RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JIE M., JOHNSTON L.,
 RA JONES M., KERSTAM J., KIRSTEN J., LAISTER J., LATREILLE P.,
 RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PASONS J., PEECY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.:
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.*;
 RL Nature 368:32-38(1994).
 RL [2].
 RP Nature 368:32-38(1994).
 RA SEQUENCE FROM N.A.
 RA HALLSWORTH K.:
 RL Submitted (Dec-1995) to the EMBL/GenBank/DBJ databases.
 RN [3].
 RN SEQUENCE FROM N.A.
 RP WATERSTON R.:
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U61547; AAA83194.1; ..
 SO PRAM: PR00178; EEs; 1.6198 MW; 9806767E CRC32;
 SO SEQUENCE 532 AA; 60198 MW; 9806767E CRC32;

[illegible]

Query Match	Best Local Similarity	Score	DB 4	Length	DB 11	Score	DB 12	Length	DB 13	Score	DB 14	Length	DB 15	Score	DB 16	Length	DB 17	Score	DB 18	Length	DB 19	Score	DB 20	Length	DB 21	Score	DB 22	Length	DB 23	Score	DB 24	Length	DB 25	Score	DB 26	Length	DB 27	Score	DB 28	Length	DB 29	Score	DB 30	Length	DB 31	Score	DB 32	Length	DB 33	Score	DB 34	Length	DB 35	Score	DB 36	Length	DB 37	Score	DB 38	Length	DB 39	Score	DB 40	Length	DB 41	Score	DB 42	Length	DB 43	Score	DB 44	Length	DB 45	Score	DB 46	Length	DB 47	Score	DB 48	Length	DB 49	Score	DB 50	Length	DB 51	Score	DB 52	Length	DB 53	Score	DB 54	Length	DB 55	Score	DB 56	Length	DB 57	Score	DB 58	Length	DB 59	Score	DB 60	Length	DB 61	Score	DB 62	Length	DB 63	Score	DB 64	Length	DB 65	Score	DB 66	Length	DB 67	Score	DB 68	Length	DB 69	Score	DB 70	Length	DB 71	Score	DB 72	Length	DB 73	Score	DB 74	Length	DB 75	Score	DB 76	Length	DB 77	Score	DB 78	Length	DB 79	Score	DB 80	Length	DB 81	Score	DB 82	Length	DB 83	Score	DB 84	Length	DB 85	Score	DB 86	Length	DB 87	Score	DB 88	Length	DB 89	Score	DB 90	Length	DB 91	Score	DB 92	Length	DB 93	Score	DB 94	Length	DB 95	Score	DB 96	Length	DB 97	Score	DB 98	Length	DB 99	Score	DB 100	Length	DB 101	Score	DB 102	Length	DB 103	Score	DB 104	Length	DB 105	Score	DB 106	Length	DB 107	Score	DB 108	Length	DB 109	Score	DB 110	Length	DB 111	Score	DB 112	Length	DB 113	Score	DB 114	Length	DB 115	Score	DB 116	Length	DB 117	Score	DB 118	Length	DB 119	Score	DB 120	Length	DB 121	Score	DB 122	Length	DB 123	Score	DB 124	Length	DB 125	Score	DB 126	Length	DB 127	Score	DB 128	Length	DB 129	Score	DB 130	Length	DB 131	Score	DB 132	Length	DB 133	Score	DB 134	Length	DB 135	Score	DB 136	Length	DB 137	Score	DB 138	Length	DB 139	Score	DB 140	Length	DB 141	Score	DB 142	Length	DB 143	Score	DB 144	Length	DB 145	Score	DB 146	Length	DB 147	Score	DB 148	Length	DB 149	Score	DB 150	Length	DB 151	Score	DB 152	Length	DB 153	Score	DB 154	Length	DB 155	Score	DB 156	Length	DB 157	Score	DB 158	Length	DB 159	Score	DB 160	Length	DB 161	Score	DB 162	Length	DB 163	Score	DB 164	Length	DB 165	Score	DB 166	Length	DB 167	Score	DB 168	Length	DB 169	Score	DB 170	Length	DB 171	Score	DB 172	Length	DB 173	Score	DB 174	Length	DB 175	Score	DB 176	Length	DB 177	Score	DB 178	Length	DB 179	Score	DB 180	Length	DB 181	Score	DB 182	Length	DB 183	Score	DB 184	Length	DB 185	Score	DB 186	Length	DB 187	Score	DB 188	Length	DB 189	Score	DB 190	Length	DB 191	Score	DB 192	Length	DB 193	Score	DB 194	Length	DB 195	Score	DB 196	Length	DB 197	Score	DB 198	Length	DB 199	Score	DB 200	Length	DB 201	Score	DB 202	Length	DB 203	Score	DB 204	Length	DB 205	Score	DB 206	Length	DB 207	Score	DB 208	Length	DB 209	Score	DB 210	Length	DB 211	Score	DB 212	Length	DB 213	Score	DB 214	Length	DB 215	Score	DB 216	Length	DB 217	Score	DB 218	Length	DB 219	Score	DB 220	Length	DB 221	Score	DB 222	Length	DB 223	Score	DB 224	Length	DB 225	Score	DB 226	Length	DB 227	Score	DB 228	Length	DB 229	Score	DB 230	Length	DB 231	Score	DB 232	Length	DB 233	Score	DB 234	Length	DB 235	Score	DB 236	Length	DB 237	Score	DB 238	Length	DB 239	Score	DB 240
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Query Match	15.9%	Score 283	DB 6	Length 336
Best Local Similarity	29.2%	Pred. No. 9.2e-18		
Matches 84	Conservative 43	Mismatches 115	Indels 46	Gaps 9
QY 78	POASSREPPPEPCPYIDQAPAGSDLVDPGGTLTBHSHLEQVSNVGEVLADIETIA	137		
DB 8	PRAHAAEPAHLVEEAHYI-----TLDGTRKHTTIDSETSEQYTRMAA--ALEGYRKE	58		
QY 138	CLLNLITADPMQSPSNQWMLTTEHORYRLRPMGKARQELGKELCANSEQFMRSP	197		
DB 59	QERLTIPIPIPIWISDQVLAHVVYVWPKESMTDHLTLNLISGRELCSISQDFORVP-	118		
QY 198	GGDVLAHLIDWKSAAWKKR-----TSPGAIHYCASTSEBSW	235		
DB 118	REELIWSHLELRKYVLA SEQOMNEIYTIIDPQCIIPASVQATPTAIKAINISAKAAK	177		
QY 236	TD-----SEVDSGCCGQ-----PIHLOFLKELLKHSYGRFRWLNKEGIRKIDS	284		
DB 178	VQAPRPISEDSSSGPNRTGNNGQIQLOWQFLLELTLDKARD-CISWQDE-GEFKLNOP	235		
QY 285	AGVAAELIRKRRPAMNYDKLSRSIROYYKGIIRKPDISORLYQV 332			
DB 236	ELVAAKMGQRKKPKPTMYNTEKLSRAJRYYYDDGMICKVQ-GKAFYVKFV 282			
RESULT 6				
ID 062804	PRELIMINARY:	PRT:	336 AA.	
AC 062804:				
DT 01-AUG-1998	(TREMBLrel. 07, Created)			
DT 01-AUG-1998	(TREMBLrel. 07, Last sequence update)			
DT 01-MAY-1999	(TREMBLrel. 10, Last annotation update)			
DE TRANSCRIPTION FACTOR GABP ALPHA SUBUNIT (FRAGMENT).				
OS Ovis aries (Sheep).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;				
OC Caprinae; Ovis.				
RN (1)				
RP SEQUENCE FROM N.A.				
RA EKASHI T., EALY A.D., OSTROWSKI M.C., ROBERTS R.M.;				
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.				
DR EMBL, AF037717; AAC39262.1; ..				
DR PFWA; PF00178; Ecs; 1.				
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.				
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.				
DR NON TER 1				
SO SEQUENCE 336 AA; 38033 MW; 8CFE91F CRC32;				

RA MEDLINE: 98358003.
 RA MAGER A.M., GRAPIN-BOTTON A., LADJALI K., MEYER D., WOLFF C.M.,
 RA STIGLER P., BONNIN M.A., REMY P.:
 RT "The avian fil gene is specifically expressed during embryogenesis in
 RT a subset of neural crest cells giving rise to mesenchyme."
 RL Int. J. Dev. Biol. 42:561-572(1998).
 DR EMBL: Y14773; CAA75077.1;
 DR EMBL: Y14774; CAA75078.1;
 DR PFAM: PF00178; Ets: 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
 SO SEQUENCE 432 AA; 48761 MW; 8f0117BD CRC32;

Query Match 15.4%; Score 274; DB 13; Length 432;
 Best Local Similarity 34.8%; Pred. No. 8.3e-17;
 Matches 77; Conservative 31; Mismatches 75; Indels 38; Gaps 9;

QY 143 ITADPMDSPPSVQKWLMTHEOYRLPPGKA-FOELAGKEICAMSEDF-RQSPGLGD 200
 DB 126 VPADPLMTQEHVROWLEWAIKEYGIMEIDTFFQNMCKELCKNNKDDFLRTSLYTE 185
 QY 201 VLAHLIDIKSAAMKERSPAIHICAS-----TSEESW----- 236
 DB 186 VLLSHLYRESSSLAYNTPS--HTEASSRLATEGPPVACTONVTKTEQRPQDPY 243
 QY 236 -----TDSEVDSGSGOPILHMOFLKELLKPHSYGREFIRMLNKEGFKIEDSAQVRL 290
 DB 244 QILGFTSSRLANPGSG-QIQMQFLF-LLSGSSNASCTIT-EGNGEFKMTDPEVARR 300
 QY 291 WQIRKNRPAMNTDKLSRSIRYOYKGIIRKPDISQRLVYQF 331
 DB 301 WGRKSKPMNYDKLSRLALRYYYDKRMVTKVH-GKRAYKF 340

RESULT 8
 QYH25 PRELIMINARY; PRT; 435 AA.
 AC QYH25:
 DT 01-MAY-1999 (TREMELREL. 10, Created)
 DT 01-MAY-1999 (TREMELREL. 10, Last sequence update)
 DT 01-MAY-1999 (TREMELREL. 10, Last annotation update)
 DE E74-LIKE FACTOR-1.
 GN ZER1.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
 CC Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae;
 CC Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RA UCHIDA H., ZON L., MIYAZAKI Y., NIMER S.;
 RT "Cloning of several members of the Ets family of proteins from
 RT zebrafish."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U84615; AAD04753.1;
 DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
 SO SEQUENCE 435 AA; 48339 MW; EC9CECF4 CRC32;

Query Match 14.9%; Score 265.5; DB 13; Length 435;
 Best Local Similarity 30.1%; Pred. No. 4.9e-16;
 Matches 84; Conservative 47; Mismatches 91; Indels 57; Gaps 12;

QY 88 EEPQCP-VIDSQAPAGSLDVPGLTLEHRS---LEVOQSNV---VGEV----- 131
 DB 26 DDPEVPAVIVEQVPADLMQVYSGLEADEVTNGINVDALQDVYEEEMGDDVGLSVETPV 85
 QY 131 -----LKDITACKLINITADPMDSPPSV--QKWLMTHEOYRLPPGKAFOELAGKE 182
 DB 86 SGGEDNMTETEAFAALLNME-----SPNNILDEKRIHT-----YGNLTETD 127

QY 183 LCMSEDFRQSPGLGDVH-----AHLD-----IKSAAWKERTSPGAIHYCASTSE 232
 DB 128 LSYISLRP--EHLNGMDVAHDETSLLDEVPQKNFSKPARKTKVR-KRPAPPCPIIN 184
 QY 233 ESWTDEVDSSGSGOPILHMOFLKELLKPHSYGREFIRMLNKEGFKIEDSAQVRLNG 292
 DB 185 PSLPLKRSKSGKNTIYLBELFALLQDKNCTCPKIKTKOREKGIKFLVDSKAASVLMG 244
 QY 293 IRKNRPAMNTDKLSRSIRYOYKGIIRKPDISQRLVYQF 331
 DB 245 KHKNKPMNYETMGRLALRYYYORGILAKVE-GQRLVYQF 282

RESULT 9
 Q15723 PRELIMINARY; PRT; 581 AA.
 AC Q15723:
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-MAY-1999 (TREMELREL. 10, Last annotation update)
 DE ETS TRANSCRIPTION FACTOR.
 GN NERF-2.
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN, FETAL LIVER, FETAL BRAIN;
 RX MEDLINE: 96347578.
 RA OETGEN P., AKBARALI Y., BOLTAX J., BEST J., KUNSCHE C.,
 RA LIBERMAN T.A.;
 RT "Characterization of NERF, a novel transcription factor related to
 RT the Ets factor E1F-1."
 RL Mol. Cell. Biol. 16:5091-5106(1996).
 DR EMBL: U43188; AAB37759.1;
 DR PFAM: PF00178; Ets: 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
 SO SEQUENCE 581 AA; 62711 MW; 2EE2228A CRC32;

Query Match 14.4%; Score 257; DB 4; Length 581;
 Best Local Similarity 25.5%; Pred. No. 4.2e-15;
 Matches 77; Conservative 50; Mismatches 97; Indels 78; Gaps 9;

QY 45 PSPAPPEGLSFLYSTDMLY-PEDSSMAKAGASREPEPEPQCPYIDS----- 99
 DB 39 PVPARLEQGYAAQVLYYDDEYMMQDVA-----EEOEVETENVEVEVASHS 87
 QY 99 -----QAPAGSLDVPGLTLEHSLLEVOQSNVGVGVKDIETACKLINTADPM 149
 DB 88 NAHCTDKTEALMALHMSFCLDRSPEFIHAAMPDY--TETVEVSTESSEPM 145
 QY 150 WSPSNQKWLMTHEOYRLPPGKAFOELAGKEICAMSEDFRQSPGLGDVLAHLIDW 209
 DB 146 TSP-----IPSPDSHEPMKKK--YVRKPKTOQSPISNG----- 179
 QY 210 KSAAMKERTSPGAIHYCASTSESWTSEVDSSGSGPILHMOFLKELLKPHSYGFI 269
 DB 179 SPGLKTKKPRG-----KGTITLMEFLDLDDCKNTCPYI 216
 QY 270 RVLNKEGFKIEDSAQVRLNGIRKNRPAMNTDKLSRSIRYOYKGIIRKPDISQRLVY 329
 DB 217 KTOREKGIKFLVDSKAASVLMGKHKRPNMNYETMGRLALRYYYORGILAVE-GQRLVY 275

RESULT 10
 Q70273 PRELIMINARY; PRT; 300 AA.
 ID Q70273

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AC 070273; 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ETS HOMOLOGOUS FACTOR (EHF) (EHF).
GN EHF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTARY;
RX MEDLINE: 98262938.
RA BOCHERT M.A., KLEINBAUM L.A., SUN L.Y., BURTON F.H.;
RT "Molecular cloning and expression of Ehf, a new member of the ets
RT transcripion factor/oncoprotein gene family.";
RL Blochem. Biophys. Res. Commun. 246:176-181(1998).
DR EMBL: AF035527; AAC40119.1; -.
DR MCD: MGI:1270840; EHF.
DR PFM: PFM0178; Ets; 1.
DR SEQUENCE 300 AA; 34903 MW; 383FE2B6 CRC32;

Query Match 14.4%; Score 236.5; DB 11; Length 300;
Best Local Similarity 28.0%; Pred. No. 1.9e-15;
Matches 69; Conservative 47; Mismatches 65; Indels 65; Gaps 9.

Oy 147 PMDMSNVOKLWTEHOYRLPPMKAPQE--LAKGELCAASEQFRORSPGSGVLA 204
Db 47 POYWKRYQWEMHLDPDNOADACIPREDISEHLCSSLOEFTTAASAGOLYS 106
Oy 205 HL-----DIWKS----AMKERTSPQAIHYCASTSESWT-----DSEVD---- 242
Db 107 NLOHLKMWGOCSSDLFOSAHNYIVYEQDPSIMN---TWKEENLYDPSYSTVDLDS 163
Oy 242 -SSSCGQ-----PI-----HMOPLKEHLKPHSY 265
Db 164 KTFCAQJISMTSSHLPAVASEPDMKKEQDPKSHTKKKNPBGTHLMETIRDLISPKN 223
Oy 266 GREIWLKNEKGIPIEDSAQYARLWGRINRPNAMNYDKLSIRQYKGIIRKPDISQ 325
Db 224 PGLIMWEDSESGIFFLKSEAVAQLMGKKNNSSMYEKLSPAMRYRYREILERVD-GR 282
Oy 326 RLVPQF 331
Db 283 RLVPKF 288

RESULT 11
O9YHUS PRELIMINARY: PRT: 440 AA.
AC O9YHUS.
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE TRANSCRIPTION FACTOR E4F1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
OC Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE: 98252138.
RA VILLARD L., TASSONE F., CRNOGORAC-JUNCEVIC T., CLANCY K.,
RA GARDINER K.;
RT "Analysis of pufferfish homologues of the A-trich human APP gene.";
RL Gene 210:17-24(1998).
RN (2)
RP SEQUENCE FROM N.A.
RA TASSONE F., VILLARD L., CLANCY K., GARDINER K.;
RT "Structure, sequence characteristics, and synteny relationships of
RT the transcription factor E4F1, the splicing factor UAF35 and the
RT crystallin beta-synthetase genes from Fugu rubripes.";
```

Query Match 14.3%; Score 255.5; DB 13; Length 440;
Best Local Similarity 24.6%; Pred. No. 4e-15;
Matches 78; Conservative 50; Mismatches 110; Indels 79; Gaps 8;

DR Gene 226:211-223 (1999).
RL EMBL: AF090120; AD13395.1;
SO SEQUENCE 440 AA; 49595 MW; 0E3E74F6 CRC32;

QY 60 LSYDMLTPEDSSMAAKAPGASSREPEPEEQPVDSQ--APAGSLDYPGGILTEEH 117
Db 107 LNIETVPRVTEVEVIDPDPAAGEGALVEGOIIVERSLSDEASQVRRMAALGGY 166
QY 118 SLEQVQSVWVEVLMDIETACKLINTADPMDMSPSNQKMLWTEHOYRLPMPKAEQE 177
Db 167 RKEQVR-----LQIPDPVLMSADQYIHNAVWYMKRFNIDEMIGSIH 209
QY 178 LAGELKAMSEEQEQRKSPGLGDVLAHLADIMKSAAMKERTSPGAIHYCASTSESTWD 237
Db 210 IPRGLICFSFOEEFLQKVP-NGEILMSHLELLRK-----YVLASQDSQSGD 254
QY 238 SEV-----DSSCSGQ-----PIHLMQFL 255
Db 255 AVTIIDQVQIIPPOVNTPTIAIKVLKQSGRPAPRPISEESSSPGNRGNGQIOMQFL 314
QY 256 KELLKPHSYGRFIRMNLKRGKIFKIEDSAQVARIKGRNRPANMYDKLSRSIROYKK 315
Db 315 LELLTDKDA--RDCIYRGEGEGEFLNQLPELVAQKRWGQRKNKPTWNYEKLSBALRYYYDG 372
QY 316 GIIRKPDISORLYYQFV 332
Db 373 DMISKVQ-GKRFVKNFV 388

RESULT 12
ID 017057 PRELIMINARY: PRT: 481 AA.
AC 017057;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE C24A1.2 PROTEIN.
GN C24A1.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
CC Rhabditina; Rhabditoidae; Rhabditidae; Peloderiinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RX WILSON R., ANSCOUGH R., ANDERSON K., BAYNES C., BEKS M.,
BOUFFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUREIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JIER M., JOHNSTON L.,
JONES M., KEESHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRI-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.*;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA CONNELL M.;
RL submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA WATERSTON R.;
RL submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Carnivora; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97050779.
 RA MIYAZAKI Y., SUN X., UCHIDA H., ZHANG J., NIMER S.;
 RT "MEF, a novel transcription factor with an Elf-1 like DNA binding
 domain but distinct transcriptional activating properties.";
 RL Oncogene 13:1721-1729(1996).
 DR EMBL: U32645; AM53693.1; -.
 DR PIRAM: PF00176; EMB: 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 SO SEQUENCE 663 AA; 70729 MW; D8CC9B7 CRC32;

Query Match 13.7%; Score 245; DB 4; Length 663;
 Best Local Similarity 27.2%; Pred. No. 6.1e-14;
 Matches 86; Conservative 47; Mismatches 103; Indels 80; Gaps 12;
 QY 66 LYPRESSAAKAPGASSEPEPEPEOC-VIDSQAPAGSLDVGGLTEF-HS----- 119
 DB 5 LQPSDLIEFASNGMDDIHOLEDPSPVAVTEQVPPLDLHLTSGLELDVHNGITD 64
 QY 119 ----LEQVSMVVGELKD-----IETACKLINTADPMDSPSNV--OKMLWTEH 164
 DB 65 GLTCHTQOILEGSFLITDDNATSHMTSTAVLME-----SPSDIDDKOIFSTSE 118
 QY 165 -----OYRLPPM-----GKAFOLACKELCANSEDFRORS 195
 DB 119 MLPDSDPAPAVTLPPVLPFAPSEPDALNRAGDTSQEGHSLSEKASRESAKTKGSKRR- 178
 QY 196 PLGGVGLAHLDIKMSAAMKERTSPGAIHYCASTSESWDSSESCSGPIHLNQL 255
 DB 178 -----IRKTKG--NRSTSP-----VTDSIPIRKSKDQKSTITLWEL 215
 QY 256 KELLKPHSYGRFIRMLNKEKGFIEDSAOYARLGLGIRKNRPNANYSIRIQYTK 315
 DB 216 LALLDNRNCPYIKYIKWTGREKIFRLVDSKAVSKLMGKOKNPNDEYEMGALAYTOR 275
 QY 316 GIIRKPDISQRLVYQF 331
 DB 276 GILAKVE-GQRLVYQF 290

Search completed: November 21, 1999, 02:06:12
 Job time: 833 sec

GenCore version 4.5
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OM protein - protein search, using sw model
 Run on: November 21, 1999, 01:52:19; Search time 16.06 seconds
 (without alignments)
 1283.756 Million cell updates/sec

Title: US-09-126-945-2
 Perfect score: 1785
 Sequence: 1 MGSASPGLSVSPSHLLPP.....GIIRKPDISQRLVYQFVHPDI 335

Scoring table: BIOSUM62

Searched: 201082 seqs, 61543640 residues

Database:

SPTREMBL.10:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_protist:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	1785	100.0	335	4	095238 homo sapien
2	487.5	27.3	363	5	097145 strongyloce
3	417	23.4	532	5	019695 caenorhabdi
4	299	16.8	255	4	095175 homo sapien
5	288	16.1	253	11	0922K6 mus musculu
6	283	15.9	336	6	062804 ovis aries
7	274	15.4	432	13	093425 colurnix co
8	265.5	14.9	435	13	091H25
9	257	14.4	581	4	015723
10	256.5	14.4	300	11	070273 mus musculu
11	255.5	14.3	440	13	09YHUS
12	252.5	14.1	481	5	017057
13	249.5	14.0	385	4	014319
14	249	13.9	348	4	099718 homo sapien
15	245	13.7	663	4	099607 homo sapien
16	245	13.7	663	4	060435 homo sapien
17	245	13.7	426	6	062803
18	242	13.6	521	4	015725
19	242	13.6	655	11	0922U4
20	241	13.5	533	4	015724
21	239	13.4	471	13	057566
22	238.5	13.4	371	4	P78545
23	235.5	13.2	371	11	035275 mus musculu
24	230.5	12.9	490	13	09YH24
25	229	12.8	494	13	057586
26	225	12.6	390	13	091RW8
27	224	12.5	95	4	095058
28	221	12.4	336	13	09YHMS
29	219	12.3	454	4	075849

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30 218.5 12.2 441 5 027378
31 218 12.2 428 4 075606
32 213.5 12.0 477 13 09YHW6
33 212.5 11.9 477 13 093322
34 209.5 11.7 236 13 09YHW7
35 207 11.6 788 5 096416
36 203 11.4 538 5 093320
37 201.5 11.3 559 5 026645
38 197.5 11.1 268 13 091744
39 191 10.7 196 4 016203
40 185 10.4 254 4 016199
41 184 10.3 377 5 022355
42 182.5 10.2 340 11 070132
43 179 10.0 238 4 099581
44 176 9.9 208 5 018579
45 155.5 8.7 256 13 042415
042415 gallus gall

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ALIGNMENTS

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RESULT 1
ID 095238 PRELIMINARY: PRT: 335 AA.
AC 095238:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE ETS TRANSCRIPTION FACTOR PDEF.
GN PDEF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA OETGEN P., FINGER E., AKBARALI Y., THAMRONGSAK U., DUBE A.,
RA BOLJAK J., BROWN L., KUNSCH C., LIBERMANN T.A.;
RT "Isolation and characterization of a novel prostate
RT epithelium-specific Ets transcription factor, PDEF."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF071538; AAC95296.1; -.
SQ SEQUENCE 335 AA: 37517 MW: 8744508 CRC32:

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Query Match 100.0%; Score 1785; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 4, 4e-153;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MGSAPGSLSSVPSHLLLPDVTSTGLEKAAAGVGLERDMSPPATPEOGLSAFYLL 60
DB 1 MGSAPGSLSSVPSHLLLPDVTSTGLEKAAAGVGLERDMSPPATPEOGLSAFYLL 60
OY 61 SYFDMLYPEDSSWAKAKAGASSREPEPEPCPIYDSQAPAGSLDLYPGSLTEESLE 120
DB 61 SYFDMLYPEDSSWAKAKAGASSREPEPEPCPIYDSQAPAGSLDLYPGSLTEESLE 120
OY 121 QVQSVNVEEVLKDIETFAKLLNTTADPMWSPSVQKLLMTEHQYRLPMGKAFQELAG 180
DB 121 QVQSVNVEEVLKDIETFAKLLNTTADPMWSPSVQKLLMTEHQYRLPMGKAFQELAG 180
OY 181 KELCAMSEGEFRORSPLGGDVLHAHLDIWKAAMKERTSPGATHYCASTSESWTSEV 240
DB 181 KELCAMSEGEFRORSPLGGDVLHAHLDIWKAAMKERTSPGATHYCASTSESWTSEV 240
OY 241 DSSCGGPIHLMQFLKELLLPHSYGRFIRWLNKKEGIFKIEDSAQYARLWGIKRNPNAM 300
DB 241 DSSCGGPIHLMQFLKELLLPHSYGRFIRWLNKKEGIFKIEDSAQYARLWGIKRNPNAM 300
OY 301 NYDKLSIRQYKKGIIKRPDISORLYOVFHPH 335
DB 301 NYDKLSIRQYKKGIIKRPDISORLYOVFHPH 335

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RESULT 2
ID 097145 PRELIMINARY: PRT: 363 AA.
AC 097145:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE ETS TRANSCRIPTION FACTOR.
GN ETS4.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
OC Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
RN [1]
RP SEQUENCE FROM N.A.
RA WEI Z., ANGERER R.C., ANGERER L.M.;
RT "Identification of a new sea urchin ets protein, SPets4, by yeast
RT one-hybrid screening with the hatching enzyme promoter."
RL Mol. Cell. Biol. 0:0-0(1999).
DR EMBL: AF106964; AAD19942.1; -.
SQ SEQUENCE 363 AA: 40768 MW: C4B9BDEFA CRC32:

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Query Match 27.3%; Score 487.5; DB 5; Length 363;
Best Local Similarity 30.8%; Pred. No. 3, 8e-36;
Matches 119; Conservative 57; Mismatches 105; Indels 105; Gaps 9;

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OY 8 LSSVPSHLLLPDVTSTGLEKAAAGVGLERDMSPPSP-----PATPE-OGLSAFY 59
DB 23 LAEISMOSTLIDLIDLOOQ-----ORNGSPSPSPGGFGLPPSPMOG----- 66
OY 60 LSYFDMLYPEDSSWAKAKAGASSREPEPEPCPIYDSQAPAGSLDLYPGSLTEESLE 119
DB 66 -----SYFQNFPPFQOMGSTIIOO-----GNGQISEEE 96
OY 120 EOVQSVNVEEVLKDIETFAKLLNTTADPMWSPSVQKLLMTEHQYRLPMGKAFQEL 179
DB 97 NEMRLIMREMIDILEDCHKLLINLVYCAWPEDEVQKLLCVANRFELGELMCHFIYN 156
OY 180 GRKLCAMSEGEFRORSPLGGDVLHA-----HLDIKSAAMKERTSPG--AIHY- 227
DB 157 GPTLATLQVDVDFHRAPKCGDILYSVCLLKSSIHFDVAPQVVPQAOQMPNIPQSPHI 216
OY 227 -----CASTSESWTSEVSSCGP----- 249
DB 217 TGAFTTMMPRKTYTPVSPVATPGDESGTSPSODELSTSPAPSGNTSMTPNHTGG 276
OY 249 IHLMOFLKELLLPHSYGRFIRWLNKKEGIFKIEDSAQYARLWGIKRNPNAMNDKLSRS 308
DB 277 IOLMOFLKELLLQPNYSYCIIMIDRTOGIFKIEDSEVEARLWGIKRNPNAMNDKLSRS 336
OY 309 IROYKKGIIKRPDISORLYOVFHP 334
DB 337 IROYKKGIIKRPDISORLYOVFHP 362

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RESULT 3
ID 019695 PRELIMINARY: PRT: 532 AA.
AC 019695:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE SIMILAR TO DNA BINDING PROTEIN.
GN F22A3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdilitia; Rhabdilitida;
OC Rhabdilitia; Rhabdilitidae; Rhabdilitidae; Peloderinae; Caenorhabdilita;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERS M.,

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RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOMMEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SUTLSON J.,
 RA THERRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROUT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."*
 RL Nature 368:32-38(1994).
 RN
 RP SEQUENCE FROM N.A.
 RA HALLSWORTH K.:
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA WATERSSTON R.:
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41547; AAA83194.1; -.
 DR PFAM: PF00178; Ets; 1.
 SQ SEQUENCE 532 AA; 60198 MW; 9806767E CRC32;

Query Match 23.4% Score 417; DB 5; Length 532;
 Best Local Similarity 24.1% Pred. No. 1.4e-29;
 Matches 127; Conservative 63; Mismatches 118; Indels 218; Gaps 16;

OY 4 ASPGSLVSPSHLLPPTVSRITGLEKAAAGAVGER---DMSPSPARPE----- 53
 DB 27 ASPGSLVSPSHLLPPTVSRITGLEKAAAGAVGER---DMSPSPARPE----- 53
 OY 53 ---OGLSAFYLSYFDMLY-----PEDSS-----AAKAPGASGREP---DEE 89
 DB 73 TOFHGLNOFAFPFNLLEYKSGCKSDSSMNGTSGVGRHNSLSF-----EPHSGTES 126
 OY 90 PEGCPVDSQAPAGSLD-----VPGGLTLE-----EHS----- 119
 DB 127 TASTPFVKESEPFDD-DLFGIDQVNNVKKPHRPMDCNLPIDPIEYNNRPSKADHSTYVK 185
 OY 119 -----LEQVQSMVYGEVLEKDIETACKLNTADPMDS 152
 DB 186 NEIEENILNFNVPRIADNGIDQIDIRLIRHLIDISTCALGLPNDYLMSS 245
 OY 133 SNVQWMLMTEHOYRLPPGKAFQELACKELCANSEEOFRORSPLGGVLAHLIDIMKSA 212
 DB 246 EHGARMWEMCMQFNLQPPRNC--SITGIDLGMSOKDFEMILPAGGDTLHMOLOVMTKA 303
 OY 213 -----AMMKERTSPGAIHYCASTSEES----- 235
 DB 304 FENYHPVTVVOSSGCMTAAENNMOSTNNWLASTNOTNNMAAENPNHPPNGNGYPMNS 363
 OY 235 -----WTDEYDS 242
 DB 364 MSFQOGTVLPSPNSDTSNGSSODMDDIDILHMNNSCGFSNFHNGYMSPIDA 423
 OY 243 SSGSG-----PIHNOFLKELLKPSYGFITWLNKREKGFIEEDSAOVA 288
 DB 424 MNGSEGDDDERAYTRHOGTVHLMQFIRLELDQPROYSACVWVWDDETFEISLLLA 483
 OY 289 RLWGRKRNRPANNDKLSRIROYKKGIRKPPDISQRLVYOFVHP 334
 DB 484 RHWGRKRNRSOMNYDKLSRLSROYTKKGIQKPEKKORLYVFLFP 529

RESULT 4
 ID 095175 PRELIMINARY: PRT: 255 AA.
 AC 095175:
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)

DE E74-LIKE FACTOR 5.
 GN ELF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN
 RP SEQUENCE FROM N.A.
 RA ZHOU J., NG A.Y.N., TYMMS M.J., JERMIIN L.S., SETH A.K., THOMAS R.S.,
 RA KOJA I.:
 RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
 RT Ets genes and maps to human chromosome 11p13-15, a region subject to
 RT LOH and rearrangement in human carcinoma cell lines."*
 RL Oncogene 17:0-0(1998).
 DR EMBL: AF049703; AAC79754.1; -.
 SQ SEQUENCE 255 AA; 30121 MW; 51F79A0D CRC32;

Query Match 16.8% Score 299; DB 4; Length 255;
 Best Local Similarity 33.2% Pred. No. 2.3e-19;
 Matches 70; Conservative 42; Mismatches 79; Indels 20; Gaps 4;

OY 135 ETACKLNTADPMDSPSNVQKMLMTEHOYRLPPGKAF--OELAGKELCANSEEOFR 192
 DB 39 QTAGCSYVTSVHPKRWKRWEMWLOFCDDQYKIDTNCISFCNFNISGLQCSMTQEEFV 98
 OY 193 QRSPLGGVLAHL-----DIWKAAMKERTSPGAIHYCASTSEESMTQSEV 240
 DB 99 EAAGCGEYLFILQNIPTOGYSFENDAESKATIKDADSN---CLTKSGIKSODCHS 154
 OY 241 DSSCGQPIHMOFLKELLKPSYGFITWLNKREKGFIEEDSAOVA RLWGRKRNRPAM 300
 DB 155 HSRSLQSHLMERYRDLSPENCGLLEWEDDEQGFIRVYKSEALAKMKGQKKNDRM 214
 OY 301 NYDKLSRSIROYYKKGIRKPPDISQRLVYOF 331
 DB 215 TYEKLSBALRYRYTKGILERYD--RLVYKF 243

RESULT 5
 ID 0922K6 PRELIMINARY: PRT: 253 AA.
 AC 0922K6:
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
 DE E74-LIKE FACTOR 5.
 GN ELF5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 RN
 RP SEQUENCE FROM N.A.
 RA ZHOU J., NG A.Y.N., TYMMS M.J., JERMIIN L.S., SETH A.K., THOMAS R.S.,
 RA KOJA I.:
 RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
 RT Ets genes and maps to human chromosome 11p13-15, a region subject to
 RT LOH and rearrangement in human carcinoma cell lines."*
 RL Oncogene 17:0-0(1998).
 DR EMBL: AF049702; AAC79754.1; -.
 SQ SEQUENCE 253 AA; 29971 MW; 78F2A08A CRC32;

Query Match 16.1% Score 288; DB 11; Length 253;
 Best Local Similarity 32.9% Pred. No. 2.2e-18;
 Matches 68; Conservative 43; Mismatches 82; Indels 14; Gaps 5;

OY 135 ETACKLNTADPMDSPSNVQKMLMTEHOYRLPPGKAF--OELAGKELCANSEEOFR 192
 DB 39 QTAGCSYVTSVHPKRWKRWEMWLOFCDDQYKIDTNCISFCNFNISGLQCSMTQEEFV 98
 OY 193 QRSPLGGVLAHLIDIMKSAAMW---KERTSPGAIH---CASTSEESMTQSEVSSC 244
 DB 99 EAAGCGEYLFILQNIPTOGYSFENDAESKATIKDADSN---CLTKSGIKSODCHSRT 156


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0Y 1B3 LCANSEEPORRSPGGCVLH-----AHD-----IMSAAMMERPSGAIHYCASTSE 2322
Db 128 LSYISLRP-EHLSNGMVAAHDETSLSDEVPQKNFSFPAKTYVR-KPRAPRCSPITN 164
0Y 233 ESWTDEYDSSCCGCPHLMWFLKELLKPHSYGRTIRWLNKEKGIFRIEDSAQVARNMG 2922
Db 185 PSLPLPKKSGKSGKNGTYIYLFMEFLALLDQKNTCKRYIKMTQREKGFIRKLVDSKAVSKLGM 2444
0Y 293 IRKNRPANVYDKLSRSIRQYKKKGJIKRPDLSQLYVQF 331
Db 245 KHKNKPDMNYETMGRLRYRYQRIAGLAVGE-GORLVYQF 282

RESULT 9
015723 PRELIMINARY: PRT: 561 AA.
015723
AC 015723:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1989 (TREMBLrel. 10, Last annotation update)
DE ETS TRANSCRIPTION FACTOR.
GN NERF-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Crenata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, FETAL LIVER, FETAL BRAIN.
RX MEDLINE: 96347578.
RA OETTGEN P., AKBARALI Y., BOLTAJ J., BEST J., KUNSC H C.,
RA LIBERMAN T. A.:
RT "Characterization of NERF, a novel transcription factor related to
RT the Ets factor ERF-1."
RL Mol. Cell. Biol. 16:5091-5106(1996).
DR EMBL: U43188; AAB37759.1; -.
DR PFM: PFO0178; Ets; 1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
SQ SEQUENCE 561 AA; 62711 MW; 2EE2228A CRC32:

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Query Match Similarity      14.4% Score 257; DB 4; Length 581;
Best Local Similarity      25.5%; Pred. No. 4,2e-15;
Matches 77; Conservative   50; Mismatches 97; Indels 78; Gaps 9;

Oy    45 PSPPATPECGLSAFYLFSTFDMLY-PEDSSMAKAPGASSREPPPEEOCPVIDS----- 99
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    39 PVPASRLRDEGYAAQVLVYDDERTYMMQDA-----EEQEVETENVEIVASVHS 87
      ^
Oy    99 -----QADAGSLDLVPGGLTLEBHSLEOVOSNVGEVLKDIECTACKLINTADPMD 149
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    88 NAKCTDKTEIAEALHMHESPCLNDSRSPEPIHAMRPDI--TETVEVSTESEEPMD 145
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy    150 WSPSNVQKMLLTENHOYRLPRPKGAFOELAGIELCAMSEORONSPGLGDVLHAHLDTW 209
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    146 TSP-----IPSPDSEHPKKRK---VGKRPTPOOSPISNG----- 179
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy    210 KSAAMWKERTSPGAIHYCASTSEESWTDESVSCSGOPIHLMOFKEILLPHSYGREI 269
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    179 SEDELRIKKPRGC-----KGNTTYIMEFLLDLDOKNKTCPRI 216
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy    270 RWLNKEKGI FKIEDSAOVA RLWGIRKNRPAMYDKLSRSIROYYKKGILRKPDISO RLVY 329
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    217 KWTOEKGFVKLVDSKA VSKLWGKHNNKNDMYETMGRLRYVOGRGLAKVE-GORLVY 275
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy    330 QF 331
      ||
Db    276 QF 277

RESULT 10
ID      070273 PRELIMINARY: PRT: 300 AA.
070273

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AC 070273;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, last annotation update)
DE ETS HOMOLOGOUS FACTOR (EHF). (EHF).
GN EHF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUITARY;
RX MEDLINE; 98262938.
RA BOOHERT M.A., KLEINBAUM L.A., SUN L.Y., BURTON F.H.;
RT "Molecular cloning and expression of Ehf, a new member of the ets
RT transcription factor/oncoprotein gene family.";
RL Blochem. Biophys. Res. Commun. 246:176-181(1998).
DR EMBL; AF035537; AAC40119.1; -;
DR MGD; MGI:1270840; EHF.
PRIM: PF001178; Ets: 1.
SQ SEQUENCE 300 AA; 34903 MW; 383FE2B6 CRC32;

	Query Match	14.4%	Score 266.5:	DB 11;	Length 300;	
	Best Local Similarity	28.0%;	Pred. No. 1.9e-15;			
	Matches	69;	Conservative	47;	Mismatches	65;
					IndeIs	65;
					Gaps	
OY	147 PMDMSPNVOKELLTWTEHOYLRLPMPGAKFOE--LAGKEICASEEIOFRORSPLGGDVLHA	204				
Dd	47 POYWKRYQWMEHLQLLLDTNOLDASCIPFOERDISGEHLCNSLSDEFTTAASAGGLAYS	106				
OY	205 HL-----DIWKA---AMKERTSPCAIHCASTSEEST----DSEVD----	242				
Dd	107 NLQHKLMMNGQCSDPLFGSAHNIVYTEQTDPSIMN---TWKEENLYDPDSYSTVDLLDS	163				
OY	242 -SSCGSQ-----PI-----FLMOFLKELLKLPHSY	265				
Dd	164 KTFCCAQISMSTSHLPVAESPDMKKEDODHPVKSHTKHKNNPRGTILLMERIRILLSPDN	223				
OY	266 GRIFKLNKKGKIFKIEDSAOVARLMGIIRKNPANNYDKLSIRQYYKKGIIIRKPDISQ	325				
Dd	224 PGLIMEWDSGEGIFRFLKSEAVALMGKKNNSSMTYEKLSPAMRYIKREILERVD-GR	282				
OY	326 RLVTYOF 331					
Dd	283 RLVTYKF 288					

RESULT 11	
Q9YHU5	
ID	Q9YHU5 PRELIMINARY; PRT; 440 AA.
AC	Q9YHU5;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE	TRANSCRIPTION FACTOR E4F1
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes);
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
OC	Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 98252138.
RA	VILLARD L., TASSONE F., CRNOGORAC-JURCEVIC T., CLANCY K.,
RA	GARDINER K.;
RT	"Analysis of pufferfish homologues of the AT-rich human Afp gene.";
RL	Gene 210:17-24(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	TASSONE F., VILLARD L., CLANCY K., GARDINER K.;
RT	"Structure, sequence characteristics, and synteny relationships of
RT	the transcription factor E4F1, the splicing factor U2AF35 and the
RT	cystathionine beta-synthetase genes from Fugu rubripes.";

RL Gene 226:211-223(1999).
 DR EMBL: AF090120: AAD13395.1: -
 SQ SEQUENCE 440 AA: 49595 MW: 0E3E7AF6 CRC32:

Query Match 14.3% Score 255.5; DB 13; Length 440;
 Best Local Similarity 24.6% Pred. No. 4e-15;
 Matches 78; Conservative 50; Mismatches 110; Indels 79; Gaps 8;

QY 60 LSYFMTLPEDSSNMAKPGASSREPEPEPCVIDSO--APAGSLDLYPGCITLLEH 117
 DB 107 LNIETVPEVVEVVIDPDAGEGALVEDGQLIATRSLSIDSEASQVTRMAALLEG 166
 QY 118 SLEQVSNVGEVGLKDIETACKLINTADPMWSPSNQKMLTTEHQYRLPGKAFQE 177
 DB 167 RKEQVR-----LGIPYDPLMSADQYIHNAVVMKEFNDEMEIGSIH 209
 QY 178 LAGKELCAMSEQFRQSPPLGSDVLAHLDIWKSAMKKEKTSFGALHYCASTEESWTD 237
 DB 210 IPGRDLCSFQSEELQKVP-NGEILMSHELLLR-----YVLASODQSGGD 254
 QY 238 SEV-----DSSCSGQ-----PIHLMQEL 255
 DB 255 ALVTIDOPVOIIPVOVNPFAIKVLOSRCPRAPRISEENSSFGNRTNGGQIOMQOFL 314
 QY 256 KELLKPHSYGRFIRMLNKEGKIKIEDSAOVARLWGIRKRPAMNYDKLSRSIROYKK 315
 DB 315 LELLTDKDA--RDCIYRGEGERKLNQPELVAKQWGORKKKPTMNYEKLSRALRYYYDG 372
 QY 316 GIIRPDISQRLVYQFV 332
 DB 373 DMISKVQ-GKRFVAKFV 388

RESULT 12
 ID 017057 PRELIMINARY: PRT: 481 AA.

AC 017057;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE C24A1.2 PROTEIN.
 GN C24A1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditioidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COOPER T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMBRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALON N., SMITH A., SONNHAMMER E., STADEN R., STOLSTON J.,
 RA THIERYT-MIBS J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.*
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA CONNELL M.;
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 PL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF024491: AAB70311.1: -
 DR PFM: PF00178; Ets; 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 SQ SEQUENCE 481 AA: 53773 MW: 575FABEB CRC32:

Query Match 14.1% Score 252.5; DB 5; Length 481;
 Best Local Similarity 51.1% Pred. No. 8.3e-15;
 Matches 45; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 246 GQPIHLMQFLKELLKPHSYGRFIRMLNKEGKIKIEDSAOVARLWGIRKRPAMNYDKL 305
 DB 335 GQVTLMEFLRLRLQDDQXSPRIKIDAKGIFLVDSKAVSRMGHKKPKGNYTEM 394
 QY 306 SRSIROYKKKGIIRKPDISQRLVYQFVH 333
 DB 395 GRALRYRYQRIQLQKVD-GQRLVYREVH 421

RESULT 13
 ID 014319 PRELIMINARY: PRT: 385 AA.

AC 014319;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE FLI-1.
 GN FLI-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RX MEDLINE: 93176799.
 RA KROMAS R., MAY W., DENNY C., RASKIND W., MOORE J., MAKI R.A., BECK E.,
 RA KLEMSZ M.J.;
 RT "Human FLI-1 localizes to chromosome 11q24 and has an aberrant
 RT transcript in neuroepithelioma."
 RL Biochim. Biophys. Acta 1172:155-158(1993).
 DR EMBL: M93255; AAB58480.1; -
 DR PFM: PF00178; Ets; 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 SQ SEQUENCE 385 AA: 43437 MW: 0820C243 CRC32:

Query Match 14.0% Score 249.5; DB 4; Length 385;
 Best Local Similarity 28.0% Pred. No. 1.2e-14;
 Matches 87; Conservative 40; Mismatches 107; Indels 77; Gaps 12;

QY 79 GASSEPEPEPEPCVIDSQAPAGSLDLYPGCLT-----LEHSLEQVSNVGEV 130
 DB 3 GGLAERARESPVDCV-----SKCSLTVGGSNPNPNYNSYDEKNGPPPMITTNE- 56
 QY 131 LKDIETACKLINTADPMWSPSNQKMLTTEHQYRLPGKAFQE-FOELAGKEICAMSEE 189
 DB 56 -----RNVIVPADALVQEHVROWLEAKIKEYLSLEMDTISFPQNMCKELCKNNKE 107
 QY 190 QPROSPL-GGDVYLAHL-----DIKSAAMKE 217
 DB 108 DFLRATTLTYNTEVILSHLSYRESSLANTTSHTDQSSRLSVKEDPSYSGVRGAGANN 167
 QY 218 RTSP-----GAIHYCASTSEE-----SWTSEVDSGSGPPIHLMQFLKELL 260
 DB 168 MNSGLNKPPLGAGQATISKTEQRPQDPYQIIGLPTSSRLANPSSGQ-IOLWQFILE-LL 225
 QY 261 RPHSYGRFIRMLNKEGKIKIEDSAOVARLWGIRKRPAMNYDKLSRSIROYKKGIIR 320
 DB 226 SDSANASCITW-EGTNGEFKATDPDEVARRGOKRKSPPNNYDKLSRALRYYYDKNIMTK 284
 QY 321 PDISQRLVYQFV 331

DB 285 VH-GKRAYKX 294

RESULT 14

099718 PRELIMINARY: PRT: 348 AA.
AC 099718: 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE EPIHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1A.
GN ESE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADULT LIVER, PANCREATIC CARCINOMA:
RX MEDLINE: 97378019.
RA OETTEREN P., ALANI R.M., BARCINSKI M.A., BROWN L., AKBARALI Y.,
RA BOUTAX J., KUNSCHE C., MÜNGER K., LIBERMAN T.A.;
RT Isolation and characterization of a novel epithelium-specific
transcription factor, ESE-1, a member of the ets family.
RL MOL. Cell. Biol. 17:4419-4433(1997).
DR EMBL: U73844; AAB5824.1; -.
DR PFM: PF00178; Ets: 1.
DR PFM: PF00178; Ets: 1.
SO SEQUENCE 348 AA; 39357 MW; 274B3FA2 CRC32;

Query Match 13.9%; Score 249; DB 4; Length 348;
Best Local Similarity 24.4%; Pred. No. 1.1e-14;

Matches 89; Conservative 53; Mismatches 95; Indels 128; Gaps 16;

DB 55 LSAFYLYPDMLYPEDSSMAKAPGASSREPEPEOCFVIDSOAPAGSLDVLVPGGLTL 114
DB 7 ISNIFSYFAMYSSEDSSTLASVPPA-----ATFGADLV---LTL 44
QY 115 E-EHSEVOQ-SMWVGEVLKDIETACKLNTADPMDSPSNVQKLLM--TEHOYRLP 169
DB 45 SNPOMSLTEGTEKASWICE-----QPFQMSKTQVLDISIOVEKNKIDAS 88
QY 170 PMKARFOELAGKELCAWSEOFQ-RQSPGLGVDLHML-DIMKSA-----AMM----- 216
DB 89 AIDPSSRCMDGATLCNCALELRLVFGPL-CDQLHAGLRDLTSSSDLSLWIELLEKDG 147
QY 216 ---KERTSPGAIHYCASTSESWTD-----SEVD----- 242
DB 148 RTFOEALDPGPFQSGSPFAGELDLVDVSTAGASRSSSSSDSGSDVDLPTDGKLPSPD 207
QY 242 --SSCS-----GCP-----ITHMOFLKELLKPHSYG 266
DB 208 GPRDCKKGDPRHGKRRKGRPKLSKEYWDLGKSKHAPRGTHLWEIFRDLIHPELNE 267
QY 267 RFRMLNKEKGIFKIEDSAOVARLWGIKRNRPAMNYDKLSIRIOYKKGIIRKPDISOR 326
DB 268 GLMKEMNHGCVFRLSEAVAOQLMGOKKNSNMTYEKLSRAMRYKKREILERYD-GRR 326
QY 327 LVYOF 331
DB 327 LVYKF 331

RESULT 15

099607 PRELIMINARY: PRT: 663 AA.
AC 099607: 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE MYELOID ELF-1 LIKE FACTOR.
GN MEFL.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 97050779.
RA MIYAZAKI Y., SUN X., UCHIDA H., ZHANG J., NIMER S.;
RT "MEF", a novel transcription factor with an Elf-1 like DNA binding
domain but distinct transcriptional activating properties.
RL Oncogene 13:1721-1729(1996).
DR EMBL: U32645; AAB53693.1; -.
DR PFM: PF00178; Ets: 1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
SO SEQUENCE 663 AA; 70729 MW; D88CC9B7 CRC32;

Query Match 13.7%; Score 245; DB 4; Length 663;
Best Local Similarity 27.2%; Pred. No. 6.1e-14;

Matches 86; Conservative 47; Mismatches 103; Indels 80; Gaps 12;

QY 66 LYEDSSMAKAPGASSREPEPEOCFVIDSOAPAGSLDVLVPGGLTLF-HS----- 119
DB 5 LQSDLIFFEFASNGMDDIHQLEDPSVFPAYIVEQVPPDLHLVSGLELDVHNGITD 64
QY 119 ---LEVOVSMVYGEVLKDIETACKLNTADPMDSPSNV--OKWLMTEH 164
DB 65 GTLCMTQDQILBGSFLLTDNENATSHMTAEVLNME-----SPSLIDENQISTSE 118
QY 165 -----QYRLPM-----GKAFOLAGRELCAWSEOFQRS 195
DB 119 MLPDSDPAPAVTLPNYLFPASEPDLNLRAGDTSDEGHSLSEKASREESAKTKGSKKR- 178
QY 196 PLGGDVLHMLDVKSAAMKERTSPGAIHYCASTSESWTDSEVSSGSGOPITHMOFL 255
DB 178 -----TRKKG--NRSTSP-----VDPSTIPIRKSKDGKSTIYLWFL 215
QY 256 KELLKPHSYGFRIRMLNKEKGIFKIEDSAOVARLWGIKRNRPAMNYDKLSIRIOYKK 315
DB 216 LALLQDRNCPKIKYKIQRGKIFKLVDKSAVSKLWKGKKNKPDNMYEIMGRALRYYYOR 275
QY 316 GIKRPDISORLYOF 331
DB 276 GILAYE-GORLYOF 290

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Job time: 833 sec

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